

**O'Bryen, Barbara**

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**From:** Switzer, Juliet  
**Sent:** Wednesday, February 09, 2005 4:05 PM  
**To:** O'Bryen, Barbara  
**Subject:** FW: please search

here's the sequence of I want searched:

~~aaaaatgctcgtrtatatgc~~

the case is CRFE but not in ABSS b/c the CRF is too big. you'd have to go get the CD from mark spencer, but I've already OCRed the sequence.  
thanks.

-----Original Message-----

**From:** Switzer, Juliet  
**Sent:** Wednesday, February 09, 2005 3:42 PM  
**To:** O'Bryen, Barbara  
**Subject:** please search

please search nucleotides 191-220 of seq id no 1 from 09/925065 in genseq and uspats issued and published.

results on paper is fine

thanks.

J  
Juliet Switzer  
Art Unit 1634  
phone: 571-272-753  
office: Remsen 2D75

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	146	(thiopurine with methyltransferase) or tpmt	US-PGPUB; USPAT	OR	ON	2005/02/09 15:42
L2	54	I1 same (mutation polymorphism snp)	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L3	4	I2 same intron\$3	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L4	12	(thiopurine with methyltransferase) or tpmt	DERWENT	OR	ON	2005/02/09 15:42

(FILE 'HOME' ENTERED AT 13:36:40 ON 09 FEB 2005)

STN

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:36:48 ON 09 FEB 2005

L1 1317 S THIOPURINE(3A)METHYLTRANSFERASE

L2 928 S TPMT

L3 537 S (L1 OR L2) (4A) (POLYMORPH? OR SNP OR ALLEL?)

L4 6 S L3(6A) (INTRON?)

L5 3 DUP REM L4 (3 DUPLICATES REMOVED)

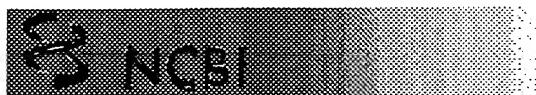
FILE 'STNGUIDE' ENTERED AT 13:40:29 ON 09 FEB 2005

L6 0 S L3 AND (ADENINE OR GUANINE)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:19:38 ON 09 FEB 2005

L7 15 S L6

L8 12 DUP REM L7 (3 DUPLICATES REMOVED)



## results of BLAST

BLASTN 2.2.10 [Oct-19-2004]

RID: 1107966805-21412-170660323395.BLAST04

**Database:** human.snp

10,022,444 sequences; 11,321,078,719 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

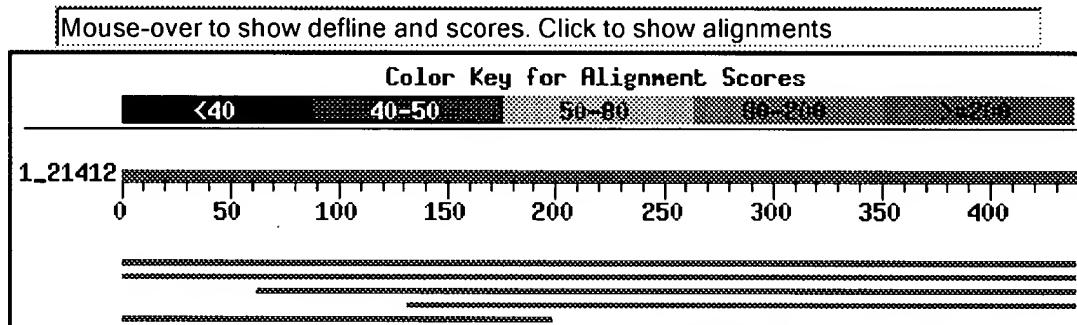
### Taxonomy reports

NO hits in prior art.

Query=

(440 letters)

### Distribution of 5 Blast Hits on the Query Sequence



Sequences producing significant alignments:		Score (bits)	E Value
gnl dbSNP rs3925948	allelePos=205totallen=440;taxid=9606;sn...	845	0.0
gnl dbSNP rs13216460	allelePos=501totallen=941;taxid=9606;sn...	837	0.0
gnl dbSNP rs2842946	allelePos=405totallen=605;taxid=9606;sn...	724	0.0
gnl dbSNP rs9367980	allelePos=500totallen=1000;taxid=9606;sn...	587	e-165
gnl dbSNP rs9465101	allelePos=151totallen=512;taxid=9606;sn...	375	e-101

## Alignments

>gnl|dbSNP|rs3925948 allelePos=205totallen=440;taxid=9606;snpClass=1;alleles='A/G';m  
      emonic;build=111  
Length = 440

Score = 845 bits (439), Expect = 0.0  
Identities = 163/440 (37%)  
Strand = Plus / Plus

```
Query: 61  nnnnnnnnnnnnnnnnnncctattgtgaactattagtatattatctagagttatgt 120
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 61  ctccatctaaaaaaaaaaacctattgtgaactattagtatattatctagagttatgt 120
```

Query: 181 ctaatctctgttaaatatgctctgttatatgctatatgctctatgttaaaggatattgaa 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 181 ctaatctctgttaaatatgctctgttatatgctatatgctctatgttaaaggatattgaa 240

Query: 421 nnnnnnnnnnnnnnnnnnc 440  
|  
Sbjct: 421 caatgcttaagctaattttc 440

bad

```
>gnl|dbSNP|rs13216460 allelePos=501totallen=941;taxid=9606;snpClass=1;alleles='G/T';  
      enomic;build=121  
      Length = 941
```

Score = 837 bits (435), Expect = 0.0  
Identities = 162/440 (36%)  
Strand = Plus / Minus

Query: 61 nnnnnnnnnnnnnnnnnnnnnnnncattgtgaactattatgtatattatgtatctagagttatgt 120  
Sbjct: 470 ctccatctaaaaaaaaaaacctattgtgaactattatgtatattatgtatctagagttatgt 411

Query: 121 ctataaaaattaaaagataaagaccattttattgaaagggttttatcttagaaaaggaa 180  
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 410 ctataaaaattaaaagataaagaccattttattgaaagggttttatcttagaaaaggaa 351

Query: 181 ctaatctctgttaaatatgtctgttatatatgtctatgtctatgttaaaagggtatggaa 240  
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||  
Sbjct: 350 ctaatctctgttaaatatgtctgttatatatgtctatgtctatgttaaaagggtatggaa 291

Query: 421 nnnnnnnnnnnnnnnnnnc 440  
|  
Sbjct: 110 caatgcttagctaattttc 91

```
>gnl|dbSNP|rs2842946 allelePos=405totallen=605;taxid=9606;snpClass=1;alleles='A/T';m  
      emonic;build=119  
      Length = 605
```

Score = 724 bits (376), Expect = 0.0  
Identities = 160/378 (42%)  
Strand = Plus / Minus

Query: 123 ataaaataaaaagataaagaccattttattgaaagtgtttatcttagaaaaggaact 182  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 545 ataaaataaaaagataaagaccattttattgaaagtgtttatcttagaaaaggaact 486

Query: 183 aatctctgttaaatatgtctgtatatatgtctatgttaaggatttgaann 242  
          |||||||||||||||||||||| ||||||||||||||||||||||||||||  
Sbjct: 485 aatctctgttaaatatgtctgtatatatgtctatgttaaggatttgaann 426



```
Lambda      K      H
 1.33      0.621      1.12

Gapped
Lambda      K      H
 1.33      0.621      1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 10022444
Number of Hits to DB: 6981
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 1.0e-02: 0
Number of HSP's better than 0.0 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 0.0: 0
Length of query: 440
Length of database: 11,321,078,719
Length adjustment: 25
Effective length of query: 415
Effective length of database: 11,070,517,619
Effective search space: 4594264811885
Effective search space used: 4594264811885
A: 0
X1: 13 (25.0 bits)
X2: 31 (60.0 bits)
X3: 25 (50.0 bits)
S1: 13 (25.0 bits)
```

s2: 25 (48.8 bits)